

INPUT SET: S36738.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

2
3 (1) General Information:

(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis Factor Receptor Releasing Enzyme Activity, and Methods of Use Thereof

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MORRISON & FOERSTER
- (B) STREET: 755 PAGE MILL ROAD
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: Windows
- (D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/752,639
(B) FILING DATE:
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US99/10793
(B) FILING DATE:

(A) APPLICATION NUMBER: 09/081,385
(B) FILING DATE:

(A) APPLICATION NUMBER: 08/964,747
(B) FILING DATE: 05-NOV-1997

(A) APPLICATION NUMBER: 60/030,761

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/752,639**

DATE: 01/31/2002
TIME: 04:08:58

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47 (viii) ATTORNEY/AGENT INFORMATION:
 48 (A) NAME: Wu, Frank
 49 (B) REGISTRATION NUMBER: 41,386
 50 (C) REFERENCE/DOCKET NUMBER: 22000-20577.21

51
 52 (ix) TELECOMMUNICATION INFORMATION:
 53 (A) TELEPHONE: 650-813-5600
 54 (B) TELEFAX: 650-494-0792
 55 (C) TELEX: 706141

56
 57 (2) INFORMATION FOR SEQ ID NO:1:

58 (i) SEQUENCE CHARACTERISTICS:
 59 (A) LENGTH: 4047 base pairs
 60 (B) TYPE: nucleic acid
 61 (C) STRANDEDNESS: double
 62 (D) TOPOLOGY: linear

63 (ii) MOLECULE TYPE: Genomic DNA

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

70	AAGCTTTTGT	CTTCCTTCC	CCGGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
71	CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGG	AGGGCTGGGA	GGCCGTCTGG	GGCCGGCTCC	120
72	TCCAGGCTGG	GGGCCGCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGCGGATG	GGGCCGCGCG	180
73	TGGGGCCCAG	CGGGCGGCC	TCGGGAGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGCCG	240
74	TGCGGGCGCC	AGCGCGTGG	GTGGAGGTG	CCGTCCCCCTCC	TGAGGGGCAG	CCAGTGCCTT	300
75	TGGGACCCGG	GAGCAGAGCC	CGGCCCTCCC	CAGGGCCTC	CCCCGGGGTC	TCACCGGGTC	360
76	ACCCGAGAGC	GGAGGCCCG	GCTCCGCAGA	AACCCGGGGC	GGCCGCGGGG	AAGCAGCGCC	420
77	CTCAGGCGTC	GGAGGAGCCC	CCAGAAGGAC	CTCGCGCCTT	CCCCGCCGGC	TCCGACCGCC	480
78	TGGGTCGGT	GCAGGACGGC	CCAGGCGGCC	AGGACCCCCA	AGCGCAGCTC	AGTCTGCAGG	540
79	GCACGACCCA	GAGGCCAGCA	GCACAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
80	GCTCCTGGG	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
81	CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCGG	TGGAGAAGGC	GCTGCTAGCC	720
82	AGGGGCGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
83	AGGGATAGGG	AGGGAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGGAC	CGCGGGCGCC	840
84	CTTTATTCTG	AAGCCGAATG	TGCTGCCGA	GTCCCCAGTG	ACCTAGAAAT	CCATTCAAG	900
85	ATTTTCAGGA	GTTCAGGTG	GAGACAAAGG	CCAGGCCAG	GTGAAATGT	GGCAGTGACA	960
86	GAGTATGGGG	TGAGAACCA	GGAGAGAGGA	AGTCCCCAG	GCAGATGATG	GGACAGAGAG	1020
87	CGGGGACCA	AATTTTTAA	AACGCATCTG	AGATGCCTT	GGCAGACTCA	TAGTTGTTT	1080
88	CCTTTCACGG	AGAAAGTGTG	GGCAGAAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
89	CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTTCCCTC	CCTGTCACAG	ACATGAGCCC	1200
90	TGGAGATCTG	GAATGAGGCA	GATGTGCCA	GGGAAAGCTG	ATCCGCCCG	ACCCAGGGCC	1260
91	CCCCGGGTG	CCCTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAAC	1320
92	CCGGACACGG	GTCTGTGCT	GCACCTGGCA	GTTGAGGAC	CGACACCCAC	AATGCCTAA	1380
93	GAGGTGATGA	CTGCCCTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCTGGC	TCCTGGAGAA	1440
94	GAGGGATTGA	GTGGAGTCCA	CGGGTCATGG	CCACGTCTG	GGTGTGCT	CTGAGGCAGG	1500
95	GCCCCGCTGG	GGTGAGAAGG	GGCTGGAGAC	AGGTTCTGC	CAGTTCAGCC	TCTAACCGGT	1560
96	GGTCTTCATG	CCTAGGAACC	CACTGGGGGC	TTATGAACT	GCAGGTGGCT	GAGTCCTTGC	1620
97	CATGGGGTCT	CTCCTTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGTACCCC	ACAAAGGGTC	1680
98	CCAGGTGAGG	CGGATGTGGC	CTGGCGCTGT	GTGGCTCTGG	ACCTAGTCCT	TGGGCTTGCG	1740
99	CTGGCGCCA	GGGCCTGGGC	TTGAGACAGC	TGTGACGCAG	GCAAGCCATT	TACCCCGTTT	1800

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100	GTGGGGACAT	TACATCTTCC	TAGCTTGGAA	CACACAGGCA	GCCAGGGTTG	TTATCCACAT	1860
101	TCCTCCTCCA	TGTCTTCTC	TTGAGAACTT	TTACCAAGGT	TGTCAGGAGC	TGGGCTCCAC	1920
102	CAGGGAGACT	CAAGTGGAAA	GCCCTCATCC	TTGTCCTCCA	GGAGACAGGA	AAACCTATGG	1980
103	TTACAATTCC	AGGGACAAAGA	GCGATGCATG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
104	GAGAAATCAG	AGACAGCTTC	CTGGAGGCAG	TGACACCTGG	ACAGGCTTCT	CCACAGGAGG	2100
105	AAGCGAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGAACA	GTGCGCGCAG	2160
106	AACCAACAAAC	CACCCCCCACC	CTAGGCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
107	TGACTACATA	GTTCCTCTGCT	GGATCTTAGG	TCTTGTCCCT	GGGCAGCTCT	GCTGAGACCT	2280
108	CTATGCCTGT	TCCAGGCTGC	ACCAAGGTTT	TGTGACTATT	GGTCTGGGGT	TGTTTGCAG	2340
109	CAACTGAAGT	GTTCTGTTGT	AAAACAGGCA	CTTGATTTGC	TGGAAGGAAT	GCTGTTGTT	2400
110	CTTGCTGCGA	CAAACATTGA	GCAGCATTAA	GTGGGCGGTT	TATATCTTGT	GGAGTAATGG	2460
111	GTGTTTTGTA	AGCTCTGCCT	GGGTACTGCA	CATTAAAAGG	AATATCATT	TCTGAAACAT	2520
112	TGCTATTTC	CACACCAGAA	ATCATATCCT	CTTGCTGGTC	CATGCTGAA	GACCTTACAC	2580
113	GAGAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAACATAATT	ATATCATAACA	2640
114	TTGCCGCTTT	CTCACTCTGC	TCTTTTCAT	CCTTGCCTAA	TTTCATTTC	TTCTGCTTCT	2700
115	TTGTTTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGTGG	AACATCTCGA	GGTGATGAAC	2760
116	AAGGTAGAGA	CTGAGATTGT	AGGATTAAG	GTGGTCTTGA	GCCTTTAGGA	GTTCCCTTCAC	2820
117	TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCTCA	2880
118	TTGTTGAAGA	ATCTCCATCG	TCACTACTTA	GCCTGTGCAC	CATGTGTAAGG	TAGTCCTCAC	2940
119	TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCAG	3000
120	AAACTTTATT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
121	CTTGTGCA	CTGTGGATGT	GTTGTGAAAC	TTGAAGGATG	GGAATATGGC	ATGTATCCTG	3120
122	CAGGGCTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGCTATT	TTGCTGTGGC	ATAAATCTGT	3180
123	TCCCAGAGCT	TGTCCTGTGGT	GGCACAAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTT	3240
124	GTTGATAATT	GGAAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300
125	ACATCATCAT	TCCACTTTGT	ACATATCTGT	TCTGCATGCT	TTTCTCCCTG	AAAACATTAG	3360
126	GACTCCTTGC	CAGGACGGCC	TGCAACAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
127	CAAGGTTATC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GTTGAGGCTA	TGGACAAGCT	3480
128	GTGAAACCAA	ATTGTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTTCT	GCTATTCTGT	3540
129	CATTAAAGAG	AAGGCTCTTT	GTAGTTGTAG	CAGGTAAAGG	AGATGGAAGA	GGCAGCTGGT	3600
130	TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660
131	CCCCATTCCAT	CCTGAATTTC	TGGAATGGTG	TTGCCTATAA	AAGTACTTAG	TTCAAGGTGCC	3720
132	AGCTGTCATT	ACTTCCCATT	TCCCAAACAC	TGGGCGAATC	GGCGTCTGAA	TCCAAGGGGA	3780
133	GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840
134	CCTCTTCCGT	CTCCTCAGTG	CGGGGAACAT	GTAGAGCCGG	GGGGAGACCA	GCCGAGAAGA	3900
135	CAAATCGTTG	CTTCTTCTTC	CTCCTCCCTCC	TCCCTCTCCC	ACATAGAAAC	ACTCACAAAC	3960
136	ACCCGACCAC	GGGGCCCGAGC	TACCGGGGGG	GCATCGCCGC	GGGCCCCGGGA	ACCAATTCTC	4020
137	CTGTCGGCGG	GGGGCGTCTTT	TGGATCC				4047

(2) INFORMATION FOR SEO ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

151 GGATCCAAAG GTCAAACCTCC CCACCTGGCA CTGTCCCCGG AGCGGGTCGC GCCCGGCCGG 60
 152 CGCGCGGGCG GGCCTTGGC GCCAGAACGCG AGAGCCCCCTC GGGGCTCGCC CCCCCCGCCTC 120

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153	ACCGGGTCAG TGAAAAAACG ATCAGAGTAG TGGTATTCA CCGGCGGCCG GCAGGGCCGG	180
154	CGGACCCCGC CCCGGGCCCC TCGGGGGAC ACCGGGGGG CGCCGGGGGC CTCCCACCTTA	240
155	TTCTACACCT CTCATGTCTC TTCACCGTGC CAGACTAGAG TCAAGCTCAA CAGGGTCTTC	300
156	TTTCCCCGCT GATTCCGCCA AGCCCCTTCC CTTGGCTGTG GTTTCGCTGG ATAGTAGGTA	360
157	GGGACAGTGG GAATCTCGTT CATCCATTCA TGCGCGTCAC TAATTAGATG ACGAGGCATT	420
158	TGGCTACCTT AAGAGAGTCA TAGTTACTCC CGCCGTTAC CCGCGCTTCA TTGAATTCT	480
159	TCACCTTGAC ATTTCAGAGCA CTGGGCAGAA ATCACATCGC GTCAACACCC GCCGCGGGCC	540
160	TTCCGCGATGC TTTGTTTAA TTAAACAGTC GGATTCCCCT GGTCCGCACC AGTTCTAAGT	600
161	CGGCTGCTAG GCGCCGGCCG AAGCGAGGCG CCGCGCGGAA CCGCGGCCCG CGGGGCGGAC	660
162	CCGCGGGGGG GACCGGGCCG CGGCCCCCTCC GCCGCCTGCC GCCGCCGCCG CGGCCGCGCG	720
163	CCGAAGAAGA AGGGGGAAA	739

164

(2) INFORMATION FOR SEQ ID NO:3:

165

166

(i) SEQUENCE CHARACTERISTICS:

167

(A) LENGTH: 233 base pairs

168

(B) TYPE: nucleic acid

169

(C) STRANDEDNESS: double

170

(D) TOPOLOGY: linear

171

172

(ii) MOLECULE TYPE: Genomic DNA

173

174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

175

176

177	CAAGAGTGGC GGCCGCAGCA GGCCCCCCGG GTGCCCGGGC CCCCCCTCGAG GGGGACAGTG	60
178	CCCCCGCCGC GGGGGCCCCG CGGCGGGCCG CGGCCGGCCC CTGCCGCCCC GACCCCTCTC	120
179	CCCCCGCCGC CGCCCCCACG CGGCGCTCCC CGGGGGAGGG GGGAGGACGG GGAGCGGGGG	180
180	AGAGAGAGAG AGAGAGAGGG CGGGGGGTGG CTCGTGCCGA ATTCAAAAG CTT	233

181

182

(2) INFORMATION FOR SEQ ID NO:4:

183

184

(i) SEQUENCE CHARACTERISTICS:

185

(A) LENGTH: 2998 base pairs

186

(B) TYPE: nucleic acid

187

(C) STRANDEDNESS: double

188

(D) TOPOLOGY: linear

189

190

(ii) MOLECULE TYPE: Genomic DNA

191

192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

193

194	GGATCCAAAG AATTGGCAC GAGGTAGTCA CGGCTCTTGT CATTGTTGTA CTTGACGTTG	60
195	AGGCTGGTGA GCTTGGAAA GTCGATGCGC AGCGTGCAGC AGCGTTGTA GATGTTCTGC	120
196	CCGTCAGCG ACAGCTTGGC GTGCTGGCG CTCACGGGT CCCCATACTG CAGCAGGGCC	180
197	TGGAACTGGT TGTTCTGGT GAAGGTGATG ATCTTCAACA CTGTGCCGA CTTGGAGAAA	240
198	ATCTGGTGCA GCACATCCAG GGTACAGGG TAGAAGAGGT TCTCCACGAT GATCCTGAGC	300
199	ACGGGGCTCT GCCCGGCCAT CGCCATCCCT GCATCCACGG CGCCGCCGA GGCAGCCAAG	360
200	GCCAGGTTCC CCGACTGGAC CGAGTTCACC GCCTGCAGGG CGCCTGGGC CGCGCCTGG	420
201	TTGGGAGAGC TGTCGGTCTT CAGCTCCTTG TGGTTGGAGA ACTGGATGTA GATGGGCTGG	480
202	CCGCGCAGCA CAGGGGTAC CGAGGTGTAG TAGTTCACCA TGGTATTGGC AGCCTCCTCC	540
203	GTGTTCATCT CGATGAAGGC CTGGTTTTTC CCCTTCAGCA TCAGGAGGTT GGTGACCTTC	600
204	CCAAAGGGCA GCCCCAGGGG GATGACTTCC CCCTCCGTGA CGTCGATGGG GAGCTCCGG	660
205	ATGTGGATCA CTCTAGAGGG GACGCCCTGCA CTTCGGCTGT CACCTTGAA CTTCTTGCTG	720

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206	TCATTTCCGT TTGCTGCAGA AGCCGAGTTG CTGCTCATGA TAAACGGTCC GTTAGTGACA	780
207	CAAGTAGAGA AAAGCTCGTC AGATCCCCGC TTTGTACCAA CGGCTATATC TGGAACATG	840
208	CCGTCCATGG CACACAGAGC AGACCCGCGG GGGACGGAGT GGAGGCGCCG GAATCCTGGA	900
209	GCTAGAGCTG CAGATTGAGT TGCTCGTGA GACGAAGCGC AAGTATGAGA GTGTCCTGCA	960
210	GCTGGGCCGG GCACTGACAG CCCACCTCTA CAGCCTGCTG CAGACCCAGC ATGCACTGGG	1020
211	TGATGCCTTT GCTGACCTCA GCCAGAACGTC CCCAGAGCTT CAGGAGGAAT TTGGCTACAA	1080
212	TGCAAGAGACA CAGAAAATAC TATGCAAGAA TGGGGAAACG CTGCTAGGAG CCGTGAACCTT	1140
213	CTTTGTCTCT AGCATCAACA CATTGGTCAC CAAGACCATG GAAGACACGC TCATGACTGT	1200
214	GAAACAGTAT GAGGCTGCCA GGCTGGAATA TGATGCCTAC CGAACAGACT TAGAGGAGCT	1260
215	GAGTCTAGGC CCCCAGGATG CAGGGACACG TGGTCGACTT GAGAGTGCCC AGGCCACTTT	1320
216	CCAGGCCCAT CGGGACAAGT ATGAGAAAGCT GCGGGGAGAT GTGGCCATCA AGCTCAAGTT	1380
217	CCTGGAAGAA AACAAAGATCA AGGTGATGCA CAAGCAGCTG CTGCTCTTCC ACAATGCTGT	1440
218	GTCCGCCCTAC TTTGCTGGGA ACCAGAAACA GCTGGAGCAG ACCCTGCAGC AGTTCACAT	1500
219	CAAGCTGCCG CCTCCAGGAG CTGAGAACCC CTCCTGGCTA GAGGAGCAGT GAGCTGCTCC	1560
220	CAGCCCAACT TGGCTATCAA GAAAGACATT GGGAAAGGGCA GCCCCAGGGT GTGGGAGATT	1620
221	GGACATGGTA CATCCTTTGT CACTTGCCTC CTGGCTTGGG CTCCCTTTTC TGGCTGGGC	1680
222	CTGACACCAAG TTTTGCCAC ATTGCTATGG TGGGAAGAGG GCCTGGAGGC CCAGAAAGTTG	1740
223	CTGCCCTGTC TATCTTCTG GCCACAGGGC TTCATTCCA GATCTTTCC TTCCACTTCA	1800
224	CAGCCAACGG CTATGACAAA ACCACTCCCT GGCCAATGGC ATCACTCTTC AGGCTGGGT	1860
225	GTGCTCCCTG ACCAATGACA GAGCCTGAAA ATGCCCTGTC AGCCAATGGC AGCTCTCTC	1920
226	GGACTCCCCCT GGGCCAATGA TGTGCGTCT AATACCCCTT GTCTCTCCTC TATGCGTGCC	1980
227	CATTGCAAGAG AAGGGGACTG GGACCAAAGG GGTGGGGATA ATGGGGAGCC CCATTGCTGG	2040
228	CCTTGCATCT GAATAGGGCT ACCCTCACCA TTTATTCACT AATACATTTT ATTTGTGTT	2100
229	TCTAATTAA AATTACCTT TCATCTTGCT TGATTTCTC TCAGCTAAAT TAGAAATTG	2160
230	TAGTTTTCC CCTAAAAAAAT TCAATGGCAT TCTTCTTAAAT AAATTACATT CTCTGATT	2220
231	CTTGTCAAGC TGCTTCAAGG AAATCCATGT GTTCAAAATG CTTGCTCGCA GTTTGTCCA	2280
232	TACCAAATGG TTGCTTAACC CAAATATCTG AGCAGCAAAT TGAGCTGATC CTTCTGGAGA	2340
233	AAGTACGGTT GAACAGCCAA GACCACTGGG TAGTCGAAGA GAAGACCCAA CATCCTGAAC	2400
234	TCCCCAGTCT GGTGTGAGGG GAGGACAGCT GATAACTGGA TATGCACTGT TCCCAGACAT	2460
235	CACTGGTCCC AAACCAATTAC TTCTGCCTGC CACTGCCACA AATACAGTAG GAATGCCATC	2520
236	CCCTTCATAC TCAGCTTAA CTCCTCAGAGT TTCATCTGGT CCTTTATGCG CAGATGTTAC	2580
237	TCGAAGTTCA CATGGAATGC CAAAATTCC ACAGGCCCTC TTGATTTTT CACAGTGACC	2640
238	AAGATCAGAA GTAGAGCCCA TCAACACTAC AACCTGCAC TGACTTTCTG ATTTCAAAAG	2700
239	CAACTCTACT CTCTCTGCAA CCCACTCAAA GTTTTTCTT ACCATTGGA GCCCTTCAGG	2760
240	AGTTACTTCT TTGAGGTCCC GATAAGACTG TTTGTCTTC TGTGCTGTC GATCTCCTGA	2820
241	TGGCCAGAGT CTCCAGGAAT CATTGTCAAT AACATCAGCA AGAACAAATT CTTTGGTGGT	2880
242	TACATCAACA CCAAATTCAA TCTTCATATC AACCAAGTGT A CAATTCTGGG GCAACCAGGA	2940
243	TTTCTCCAGT ATTTCAAATA TAGCCTGTGT AGCATCTCGT GCCGAATTCA AAAAGCTT	2998

244
(2) INFORMATION FOR SEQ ID NO:5:

245
246
247 (i) SEQUENCE CHARACTERISTICS:
248 (A) LENGTH: 4152 base pairs
249 (B) TYPE: nucleic acid
250 (C) STRANDEDNESS: double
251 (D) TOPOLOGY: linear

252
253 (ii) MOLECULE TYPE: Genomic DNA

254
255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

256	AAGCTTTTG TGAAAACCT AGGATATGTC CCCTCCCTCA CCACACCCAA CCCCCCGCCC	60
257	CTGCCCCAGG ACATGACGAT GCCTCACACA CACACACACA CACACATACA CACAAGGCCG	120

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